

BLAST

Basic Local Alignment Search Tool

[NCE/ BLAST/ Basic site/](#) **Formatting Results - NXBHZA2601N**

gb|AF172172.1| (483 letters)

Query ID [gb|AF172172.1|](#)
Description Medicago sativa non-symbiotic hemoglobin (MHB1) mRNA, complete cds
Molecule type nucleic acid
Query Length 483

Database Name nr
Description All GenBank+ EMBL+ DDBJ+ PDB sequences (but no EST, STS, GSS, environmental samples or phase 0, 1 or 2 HTGS sequences)
Program BLASTN 2.2.25+

Descriptions

Legend for links to other resources: UniGene GEO Gene Structure Map Viewer PubChem BioAssay

Accession	Description	Max score	Total score	Query coverage	E value	Max ident	Links
AF172172.1	Medicago sativa non-symbiotic hemoglobin (MHB1) mRNA, complete cds	893	893	100%	0.0	100%	
B1086529.1	Soybean clone JCVI-FLGm-10A5 unknown mRNA	571	571	94%	1e-159	89%	
AB233220.1	Lotus japonicus LjHb1 mRNA for nonsymbiotic hemoglobin, complete cds	527	527	95%	3e-146	87%	
AY886302.1	Gossypium hirsutum non-symbiotic hemoglobin protein mRNA, complete cds	442	442	88%	1e-120	85%	
AF323368.1	Gossypium hirsutum non-symbiotic hemoglobin class 1 (GLB1) mRNA, complete cds	427	427	88%	3e-116	84%	
AB221344.1	Alnus firma mRNA for nonsymbiotic hemoglobin, complete cds	390	390	95%	4e-105	81%	
AY224133.1	Pyrus communis non-symbiotic hemoglobin class 1 (GLB1) mRNA, complete cds	368	368	96%	2e-98	81%	
G0423619.1	Malus hupehensis non-symbiotic hemoglobin mRNA, complete cds	340	340	96%	4e-90	80%	
AY286331.1	Raphanus sativus nonsymbiotic hemoglobin mRNA, complete cds	244	244	93%	3e-61	77%	
U47143.1	Glycine max nonsymbiotic hemoglobin gene, complete cds	206	206	27%	1e-49	94%	
XM_002277395.1	PREDICTED: Vitis vinifera hypothetical protein LOC100253215 (LOC100253215), mRNA	176	176	33%	1e-40	86%	
Y00295.1	Trema tomentosa haemoglobin gene	167	167	28%	7e-38	88%	
AP010323.1	Lotus japonicus genomic DNA, chromosome 3, clone: LJ27C23, TM0891, complete sequence	163	163	23%	9e-37	92%	
AP004623.1	Lotus japonicus genomic DNA, chromosome 3, clone: LJ2701, TM0091a, complete sequence	163	163	23%	9e-37	92%	
Z09635.1	Trema orientalis hemoglobin gene	158	158	28%	4e-35	87%	
AF027219.1	Trema orientalis hemoglobin gene, complete cds	158	158	28%	4e-35	87%	
AJ131331.1	Trema virgata gene encoding hemoglobin, isolate T4	145	145	28%	3e-31	85%	
AJ131330.1	Trema virgata gene encoding hemoglobin, isolate T2	145	145	28%	3e-31	85%	
AJ131349.1	Trema virgata gene encoding hemoglobin, isolate T1	145	145	28%	3e-31	85%	

NOP

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Alignments

>gb|AF172172.1|AF172172 Medicago sativa non-symbiotic hemoglobin (MHB1) mRNA, complete
cds
Length=483

Score = 893 bits (483), Expect = 0.0
Identities = 483/483 (100%), Gaps = 0/483 (0%)
Strand=Plus/Plus

```
Query 1 ATGGGCACCTTTGGATACAAAAGGTTTCACTGAAGAACAAGAAGCTCTTGTGGTGAAGTCA 60
      |||
Sbjct 1 ATGGGCACCTTTGGATACAAAAGGTTTCACTGAAGAACAAGAAGCTCTTGTGGTGAAGTCA 60

Query 61 TGAATGCAATGAAGAAGAATTCTGCAGAGTTAGGACTAAAGCTTTTCTTGAAAATATTT 120
      |||
Sbjct 61 TGAATGCAATGAAGAAGAATTCTGCAGAGTTAGGACTAAAGCTTTTCTTGAAAATATTT 120

Query 121 GAGATTGCTCCATCAGCTCAAAAACCTTTTCTCATTCTTGAAAGATTCAAAAGTTCCTTTG 180
      |||
Sbjct 121 GAGATTGCTCCATCAGCTCAAAAACCTTTTCTCATTCTTGAAAGATTCAAAAGTTCCTTTG 180

Query 181 GAGCAAAACACCAAGCTCAAGCCTCATGCCATGTCTGTCTTTCTCATGACATGTGAATCA 240
      |||
Sbjct 181 GAGCAAAACACCAAGCTCAAGCCTCATGCCATGTCTGTCTTTCTCATGACATGTGAATCA 240

Query 241 GCCGTTCAACTGCGGAAATCCGGTAAAGTTACGGTCAGAGAATCAAGCTTGAAAAAATTA 300
      |||
Sbjct 241 GCCGTTCAACTGCGGAAATCCGGTAAAGTTACGGTCAGAGAATCAAGCTTGAAAAAATTA 300

Query 301 GGTGCTAACCATTTTAAATACGGTGTAGTAGACGAGCATTTTGAGGTGACAAAGTTTGCA 360
      |||
Sbjct 301 GGTGCTAACCATTTTAAATACGGTGTAGTAGACGAGCATTTTGAGGTGACAAAGTTTGCA 360

Query 361 CTTTGGAGACCATAAAAGAAGCAGTACCTGAAATGTGGTCACCGGCTATGAAGAATGCA 420
      |||
Sbjct 361 CTTTGGAGACCATAAAAGAAGCAGTACCTGAAATGTGGTCACCGGCTATGAAGAATGCA 420

Query 421 TGGGAGAAAGCTTATGATCAGTTGGTCAATGCAATCAAATCTGAAATGAAACCTTCCTCT 480
      |||
Sbjct 421 TGGGAGAAAGCTTATGATCAGTTGGTCAATGCAATCAAATCTGAAATGAAACCTTCCTCT 480

Query 481 TAG 483
      |||
Sbjct 481 TAG 483
```

>gb|BT096529.1| Soybean clone JCVI-FLGm-10A5 unknown mRNA
Length=751

Score = 571 bits (309), Expect = 1e-159
Identities = 412/461 (90%), Gaps = 9/461 (1%)
Strand=Plus/Plus

```
Query 18 AAA-AGGTTTCACTGAAGAACAAGAAGCTCTTGTGGTGAAGTCATGGAATG-CAATGAAG 75
      |||
Sbjct 102 AAAGAGGTTTCTCGGAAGAGCAAGAAGCTCTGGTGGTGAAGTCATGGAATGTC-ATGAAG 160

Query 76 AAGAATTCTGCAGAGTTAGGACTAAAGCTTTTCTTGAAAATATTTGAGATTGCTCCATCA 135
      |||
Sbjct 161 AAGAATTCTGCAGAGTTGGGTCTCAAGTTTTTCTTGAAAATATTTGAGATTGCTCCATCA 220

Query 136 GCTCAAAAACCTT-TTCTCATTCTTGAAGATTCAAAAGTTCCTTTGGAGCAAAA-CACCA 193
      |||
Sbjct 221 GCTCAGAAA-TTGTCTCATTCTTGAGAGATTCAACGGTTCCTTTGGAGCAAAATC-CCA 278

Query 194 AGCTCAAGCCTCATGCCATGTCTGTCTTTCTCATGACATGTGAATCAGCCGTTCAACTGC 253
      |||
Sbjct 279 AGCTCAAGCCCCATGCCGTGTCTGTCTTTGTAATGACCTGTGATTGAGCAGTTCAGCTGC 338

Query 254 GGAAATCCGGTAAAGTTACGGTCAGAGAATCAAGCTTGAAAAAATTAGGTGCTAACCATT 313
      |||
Sbjct 339 GGAAGGCCGGGAAAGTCACTGTCAGAGAATCAAACCTTGAAAAAATTAGGTGCTAACCATT 398

Query 314 TTA-AATACGGTGTAGTAGACGAGCATTTTGAAGGTGACAAAGTTTGCACCTTTTGAGAGACC 372
      |||
Sbjct 399 TTAGAA-CCGGCGTAGCAAACGAGCATTTTCGAGGTGACAAAGTTTGCACCTGTTGGAGACC 457

Query 373 ATAAAAGAAGCAGTACCTGAAATGTGGTCACCGGCTATGAAGAATGCATGGGAGAGAAGCT 432
      |||
Sbjct 458 ATAAAAGAAGCTGTACCAGAAATGTGGTCACCGGCTATGAAGAATGCATGGGAGAGAAGCT 517

Query 433 TATGATCAGTTGGTCAATGCAATCAAATCTGAAATGAAACC 473
      |||
Sbjct 518 TATGATCAGCTGGTCGATGCCATTAAATCTGAAATGAAACC 558
```

>dbj|AB238220.1| Lotus japonicus LjHb1 mRNA for nonsymbiotic hemoglobin, complete
cds
Length=486

Score = 527 bits (285), Expect = 3e-146
Identities = 402/460 (88%), Gaps = 2/460 (0%)
Strand=Plus/Plus

```
Query 23 GTTTCACCTGAAGAACAAGAAGCTCTTGTGGTGAAGTCATGGAATGCAATGAAGAAGAATT 82
      |||
Sbjct 23 GTTTCACCTGAAGAGCAAGAAGCTCTTGTGGTGAAGTCATGGAGCGTGATGAAGAAGAATT 82
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Query 83  CTGCAGAGTTAGGACTAAAGCTTTTCTTGAAAAATTTGAGATTGCTCCATCAGCTCAA 142
          |||||
Sbjct 83  CTGCTGAAGTGGGTCTCAAGCTTTTCTTGAAAAATTTGAGATTGCTCCATCAGCTCAGA 142

Query 143  AACTT-TTCTCATTCTTGAAAGATTCAAAGTTCCTTTGGAGCAAAACACCAAGCTCAAG 201
          |||||
Sbjct 143  AA-TTGTTCCTTTCTTGAGAGATTCAAAGTTCCTTTGGAGGAGAACCCCAAGCTCAAG 201

Query 202  CCTCATGCCATGTCTGTCTTTCTCATGACATGTGAATCAGCCGTTCAACTGCGGAATCC 261
          |||||
Sbjct 202  CCTCATGCCATGTCTGTCTTTGTCTGACTTGTGAATCAGCAGCTCAACTGCGGAAGGCT 261


Query 262  GGTAAAGTTACGGTCAGAGAATCAAGCTTGAAAAAATTAGGTGCTAACCATTTTAAATAC 321
          |||||
Sbjct 262  GGAAAAGTCACTGTGAGAGAATCAACCTTGAAAAAGCTAGGTGCTACCCATTATAAATAT 321

Query 322  GGTGTAGTAGACGAGCATTTTGAGGTGACAAAGTTTGCACTTTTGAGAGACCATAAAAGAA 381
          |||||
Sbjct 322  GGAGTAGTAAACGAGCATTTTGAGGTTACAAAGTTTGCACTACTGGATACCATAAAAGAA 381

Query 382  GCAGTACCTGAAATGTGGTCACCGGCTATGAAGAATGCATGGGAGAAAGCTTATGATCAG 441
          |||||
Sbjct 382  GCTGTACCTGAAATGTGGTCACCAGAGATGAAGAATGCATGGACACAAGCTTATGATCAG 441

Query 442  TTGGTCAATGCAATCAAACTCTGAAATGAAACCTTCCTCTT 481
          |||||
Sbjct 442  CTGGTCGGTGCCATTAAATCTGAAATGAAGCCATCATCTT 481

```

>gb|AY899302.1|  Gossypium hirsutum non-symbiotic hemoglobin protein mRNA, complete cds
Length=813

Score = 442 bits (239), Expect = 1e-120
Identities = 370/433 (86%), Gaps = 10/433 (2%)
Strand=Plus/Plus

```

Query 19  AAAGGTTTCACTGAAGAACAAGAAGCTCTT-GTGGTGAAGTCATGGAATGCAATGAAGAA 77
          |||||
Sbjct 69  AAAGTTTTCACTGAAGAACAAGAAGCT-TTGGTGGTCAAGTCATGGACTGTAATGAAGAA 127

Query 78  GAATTCTGCAGAGTTAGGAC-TAAAGCTT-TTCTTGAAAATATTTGAGATTGCTCCATCA 135
          |||||
Sbjct 128  GAATGCAGCTGAATTGGGTCTTAAA--TTCTTCTTGAAGATATTTGAGATTGCACCATCA 185

Query 136  GCTCAA-AAACTTTTCTCATTCTTGAAAGATTCAAAGTTCCTTTGGAGCAAAACACCAA 194
          |||||
Sbjct 186  GC-CAAGAACTATTCTCATTCTTGAGAGACTCAAATGTTCCATTGGAGCAAAACACAAA 244

Query 195  GCTCAAGCCTCATGCCATGTCTGTCTTTCTCATGACATGTGAATCAGCCGTTCAACTGCG 254
          |||||
Sbjct 245  GCTGAAGCCCCATGCCATGTCTGTCTTTGTCTGATGACATGTGAATCTGCAGTTCAACTGCG 304


Query 255  GAAATCCGGTAAAGTTACGGTCAGAGAATCAAGCTTGAAAAAATTAGGTGCTAACCATT 314
          |||||
Sbjct 305  TAAAGCAGGCAAAGTTACAGTGAGGGAATCAAATTTGAAGAAATTAGGAGCTACCCATT 364

Query 315  TAAATACGGTGTAGTAGACGAGCATTTTGAGGTGACAAAGTTTGCACTTTTGAGAGCCAT 374
          |||||
Sbjct 365  TAAGTATGGGTAGTTGATGAACATTTGAGGTAACAAATTTGCTCTTTTGAGAGCCAT 424

Query 375  AAAAGAAGCAGTACCTGAAATGTGGTCACCGGCTATGAAGAATGCATGGGAGAAAGCTTA 434
          |||||
Sbjct 425  AAAAGAAGCAGTACCAGATATGTGGTCAGATGAGATGAAGAATGCATGGGGTGAAGCCTA 484

Query 435  TGATCAGTT-GGT 446
          |||||
Sbjct 485  TGATC-GTTTGGT 496

```

>gb|AF329368.1|AF329368  Gossypium hirsutum non-symbiotic hemoglobin class 1 (GLB1) mRNA, complete cds
Length=634

Score = 427 bits (231), Expect = 3e-116
Identities = 368/434 (85%), Gaps = 10/434 (2%)
Strand=Plus/Plus

```

Query 19  AAAGGTTTCACTGAAGAACAAGAAGCTCTT-GTGGTGAAGTCATGGAATGCAATGAAGAA 77
          |||||
Sbjct 37  AAAGTTTTCACTGAAGAACAAGAAGCT-TTGGTGGTCAAGTCATGGACTGTAATGAAGAA 95

Query 78  GAATTCTGCAGAGTTAGGAC-TAAAGCTT-TTCTTGAAAATATTTGAGATTGCTCCATCA 135
          |||||
Sbjct 96  GAAAACAGCTGAATTGGGTCTTAAA--TTCTTCTTGAAGATATTTGAGATTGCACCATCA 153

Query 136  GCTCAA-AAACTTTTCTCATTCTTGAAAGATTCAAAGTTCCTTTGGAGCAAAACACCAA 194
          |||||
Sbjct 154  GC-CAAGAACTATTCTCATTCTTGAGAGACTCCAATGTTCCATTGGAGCAAAACACAAA 212

Query 195  GCTCAAGCCTCATGCCATGTCTGTCTTTCTCATGACATGTGAATCAGCCGTTCAACTGCG 254
          |||||
Sbjct 213  GCTGAAGCCCCATGCCATGTCTGTCTTTGTCTGATGACATGTGAATCTGCAGTGCAACTGCG 272

Query 255  GAAATCCGGTAAAGTTACGGTCAGAGAATCAAGCTTGAAAAAATTAGGTGCTAACCATT 314
          |||||

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Sbjct 273 TAAAGCAGGCAAAGTTACAGTGAGGGAATCAAATTTGAAGAAATTAGGAGCTACCCATTT 332
Query 315 TAAATACGGTGTAGTAGACGAGCATTTTGAGGTGACAAAGTTTGCACTTTTGGAGACCAT 374
Sbjct 333 TAAGTATGGGGTAGTTGATGAACATTTTGAGGTAAACAAAATTTGCTCTTTTGGAGACCAT 392
Query 375 AAAAGAAGCAGTACCTGAAATGTGGTCACCGGCTATGAAGAATGCATGGGGGAGAAGCTTA 434
Sbjct 393 AAAAGAAGCAGTACCAGATATGTGGTCAGATGAGATGAAGAATGCATGGGGTGAAGCCTA 452
Query 435 TGATCAGTT-GGTC 447
Sbjct 453 TGATC-GTTTGGTC 465
```

>dbj|AB221344.1| Alnus firma mRNA for nonsymbiotic hemoglobin, complete cds
Length=483

Score = 390 bits (211), Expect = 4e-105
Identities = 382/466 (82%), Gaps = 6/466 (1%)
Strand=Plus/Plus

```
Query 21 AGGTTTCACTGAAGAACAAGAAGCTCTTGTGGTGAAGTCATGGAATGCAATGAAGAAGAA 80
Sbjct 21 AGGGTTCACAGAAGAGCAAGAAGCTGTGGTGGTGAAGTCATGGAATGCAATGAAGCCTAA 80
Query 81 TTCTGCAGAGTTAGGACTAAAGCTT-TTCTTGAAAATATTTGAGATTGCTCCATCAGCTC 139
Sbjct 81 TGCTGGAGAAATTGGGTCTAAA-ATTCTTCTTGAAGATATTTGAGATTGCACCATCAGCTC 139
Query 140 AAAAAGCTTTTCTCATTCTTGAAGATTCAAAAGTTCCCTTTGGAGC-AAAACACCAAGCTC 198
Sbjct 140 AGAAGCTCTTCTCTTCTTGTGAGAGACTCAAATGTTCTCTCGAACGAAATC-CAAAGCTT 198
Query 199 AAG-CCTCATGCCATGTCTGTCTTTCTCATGACATGTGAATCAGCCGTTCAACTGCGGAA 257
Sbjct 199 AAGTCC-CATGCCATGTCTGTCTTTCTGATGACCTGTGAATCGGCAGTGCAACTCCGGAA 257
Query 258 ATCCGGTAAAGTTACGGTCAGAGAATCAAGCTTGAAAAAATTAGGTGCTAACCATTTTAA 317
Sbjct 258 AGCCGGCAAAGTTACTGTGAGAGAGTCGAGCTTGAAAAAGTTGGGTGCTGTCCACTTCAA 317
Query 318 ATACGGTGTAGTAGACGAGCATTTTGAGGTGACAAAGTTTGCACTTTTGGAGACCATAAA 377
Sbjct 318 GCATGGGGTGGTCCATGAACATTATGAGGTACAAAGTTTGCGTGTCTGGAACATATCAA 377
Query 378 AGAAGCAGTACCTGAAATGTGGTCACCGGCTATGAAGAATGCATGGGGAGAAGCTTATGA 437
Sbjct 378 GGAAGCGGTGCCAGAAATGTGGTCACCGGAGATGAAGATTGCATGGGGAGAAGCTTATGA 437
Query 438 TCAGTTGGTCAATGCAATCAAATCTGAAATGAAACCTTCCTCTTAG 483
Sbjct 438 TCAGTTGGTTGCTGCTATCAAATCTGCAATGAAGCCTTCTTCTTAG 483
```

>gb|AY224133.1| Pyrus communis non-symbiotic hemoglobin class 1 (GLB1) mRNA,
complete cds
Length=477

Score = 368 bits (199), Expect = 2e-98
Identities = 385/473 (82%), Gaps = 19/473 (4%)
Strand=Plus/Plus

```
Query 19 AAAGTTTCACTGAAGAACAAGAAGCTCTTGTGGTGAAGTCATGGAATGCAATGAAGAAG 78
Sbjct 10 AAAGTTTTCACAGAAGAACAGGAAACACTGGTGGTGAAGTCATGGGGTGTGATGAAGCAG 69
Query 79 AATTCTGCAGAGTTAGGACTAAAGCTT-TTCTTGAAAATATTTGAGATTGCTCCATCAGC 137
Sbjct 70 AATGCTGCTGATTGGGCCCTTAAG-TTCTTCTGAAGATCTTTGAAATTGCACCATCAGC 128
Query 138 TCAAAAACCTTTTCTCATTCTTGAAAGATTC-AAAAGTTCCT-TTGGAGCAA-AACACC-A 193
Sbjct 129 TCAGAAGCTGTTCTCTTTCTTGAGGGACTCTAATA-TTCCTCTT-GAG-AAGAAC-CCAA 184
Query 194 AGCTCAAGCCTCATGCCATGTCTGTCTTTCTCATGACATGTGAATCAGCCGTTCAACTGC 253
Sbjct 185 AGCTCAAGCCTCATGCCATGTCTGTATTTGTTATGACTTGTGAATCAGCAGTTCAACT-C 243
Query 254 -GGAAATCCGGTAAAGTTACGGTCAGAGAATCAAGCTTGAAAAAATTAGGTGCTAACCAT 312
Sbjct 244 AGGAAAGCAGGCAAGGTTACAGTGAGAGAGTCAACCTTGAAAAGATTAGGTGGTGTCCAC 303
Query 313 TTTAAATAC-GGTGTAGTAGACGAGCATTTTGAGGTGACAAAGTTTGCACTT-TTGAGA 370
Sbjct 304 TTCAAGT-CTGGAGTGGTAGATGAACATTATGAGGTGACCAAGTTCGCA-TTGTGGAAA 361
Query 371 CCATAAAGAAGCAGTACCTGAAATGTGGTCACCGGCTATGAAGAATGCATGGGGAGAAG 430
Sbjct 362 CCATAAAGAGGCCGTACCGGAAATGTGGTCACCGGAGATGAAGAATGCATGGGGAGAAG 421
Query 431 CTTATGATCAGTTGGTCAATGCAATCAAATCT-GAAATGAAACCTTCCTCTTA 482
Sbjct 422 CTTATGATCAGTTGGTTACTGCTATAAAAT-TAGAAATGAAGCCTCCC-CTTA 472
```

>gb|GQ423619.1| Malus hupehensis non-symbiotic hemoglobin mRNA, complete cds
Length=477

Score = 340 bits (184), Expect = 4e-90
 Identities = 380/473 (81%), Gaps = 19/473 (4%)
 Strand=Plus/Plus

```

Query   19   AAAGGTTTCACTGAAGAACAAGAAGCTCTTGTGGTGAAGTCATGGAATGCAATGAAGAAG   78
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Sbjct   10   AAAGTTTTTCACAGAAGAAGACAGAAACACTGGTGGTGAAGTCATGGGGTGTGATGAAGAAG   69

Query   79   AATTCTGCAGAGTTAGGACTAAAGCTT-TTCTTGAAA-ATATTTGAGATTGCTCCATCAG   136
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Sbjct   70   AACGTGCTGAATTGGGCCTTAAG-TTCTTCTT-AAAGATCTTTGAAATTGCACCATCAG   127

Query   137  CTCAAAAACTTTTCTCATTCTTGAAAGATT-AAAAGTTCTT-TTGAGAGCAA-AACACC-   192
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Sbjct   128  CTCAGAAGCTGTCTCTTCTTCTTGAGGGACTCTGACA-TTCTCTT-GAG-AAGAAC-CCA   183

Query   193  AAGCTCAAGCCTCATGCCATGTCTGTCTTTCTCATGACATGTGAATCAGCCGTTCAACTG   252
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Sbjct   184  AAGCTCAAGCCTCAGCCATGTCTGTATTAGTTATGACTGTGAATCAGCAGTTCAACT-   242


Query   253  C-GGAAATCCGGTAAAGTTACGGTCAGAGAATCAAGCTTGAAAAAATTAGGTGCTAACCA   311
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Sbjct   243  CAGGAAAGCAGGCAAGGTTACAGTGAGAGAGTCAACCTTGAAAAGATTAGGTGGTGTCCA   302

Query   312  TTTTAAATAC-GGTGTAGTAGACGAGCATTTTGAGGTGACAAAGTTTGCACTT-TTGGAG   369
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Sbjct   303  CTTCAAGT-CTGGAGTGGTAGATGAACATTATGAGGTGACCAAGTTCGCA-TTGTTGGAA   360

Query   370  ACCATAAAGAAGCAGTACCTGAAATGTGGTCACCGGCTATGAAGAATGCATGGGGAGAA   429
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Sbjct   361  ACCATAAAGGAGGCCTTACCGGAAATGTGGTCACCGGAGATGAAGAATGCATGGGGAGAA   420

Query   430  GCTTATGATCAGTTGGTCAATGCAATCAAATCTGAAATGAAACCTTCCTCTTA   482
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Sbjct   421  GCTTATGATCAGTTGGTTGCTGCTATAAAATCAGAAATGAAGCCTCCC-CTTA   472

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>gb|AY286331.1|  Raphanus sativus nonsymbiotic hemoglobin mRNA, complete cds
 Length=683

Score = 244 bits (132), Expect = 3e-61
 Identities = 359/466 (78%), Gaps = 25/466 (5%)
 Strand=Plus/Plus

```

Query   23   GTTTCACCTGAAGAACAAGAAGCTCTTGTGGTGAAGTCATGGAATG-CAATGAAGAAGAAT   81
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Sbjct   74   GTTT-ACAGAAGAGCAAGAAGCTCTTGTGGTGAAGTCATGGAGTGTCA-TGAAGAAAAAT   131

Query   82   TCTGCAGAGTTAGGACT-AAAGCTTTTCTTGAAAAATATTGAGATTGCTCCATCAGCTCA   140
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Sbjct   132  TCAGCTGATTGGGTCTCAAA-CTATTTCATCAAGATCTTTGAGATTGCACCAACAGCG-A   189

Query   141  AAAACTT-TTCTCATTCTTGAAAGATTCAAA-AGTTCCTT-TGGAGCAAAACACCAA-GC   196
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Sbjct   190  AGAAGTTGTTCTCGTTTTTGTAGAGACTCACCCA-TCCCTGCTG-AGCAAAAC-CCAAAGC   246

Query   197  TCAAGCCTCATGCCATGTCTGTCTTTCTCATGACATGTGAATCAGCCGTTCAACTGCGGA   256
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Sbjct   247  TCAAGCCTCATGCCATGTCTGTTTTTGTCTGTGTGTGAGTCAGCAGCACAGCTGAGAA   306

Query   257  AATCCGGTAAAGTTACGGTCA-G-AGAATCAAGCTTGAAAAAATTAGGTGCTAACCATTT   314
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Sbjct   307  AAACAGGAAAAGTTACAGTGAAGGAGA--CAACCCTGAAGAGGCTAGGAGCCAATCATTC   364

Query   315  TAAATACGGTGTAGTAGACGAGCATTTTGAGGTGACAAAGTTTGCACTT-TTGGAGACCA   373
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Sbjct   365  TAAATACGGCGTCGTTGATGAACACTTTGAGGTGACCAAGTATGCA-TTGTTGGAGACGA   423

Query   374  TAAAGAAGCAGTACCTGAAATGTGGTCACCGGCTATGAAGAA-TGCATGGGGAGAAGCT   432
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Sbjct   424  TAAAGGAGCGGTGCCGAGATGTGGTCACCGGAAATGAA-ATCTGCTTGGGGTCAGGCT   482

Query   433  TATGATCAG-TTGGT-CAATGCAATCAAATCTGAAATGAAACCTTC   476
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Sbjct   483  TATGATCACCTTGTGTC--TGCCATTAAAGCTGAAATGAAGCCTTC   526

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>gb|U47143.1|GMU47143  Glycine max nonsymbiotic hemoglobin gene, complete cds
 Length=1333

Score = 206 bits (111), Expect = 1e-49
 Identities = 127/135 (95%), Gaps = 0/135 (0%)
 Strand=Plus/Plus

```

Query   339  TTTTGAGGTGACAAAGTTTGCACTTTTGGAGACCATAAAAGAAGCAGTACCTGAAATGTG   398
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Sbjct   1034  TTTTAAGGTGACAAAGTTTGCACTGTGGAGACCATAAAAGAAGCTGTACCAGAAATGTG   1093

Query   399  GTCACCGGCTATGAAGAATGCATGGGGAGAAGCTTATGATCAGTTGGTCAATGCAATCAA   458
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Sbjct   1094  GTCACCGGCTATGAAGAATGCATGGGGAGAAGCTTATGATCAGCTGGTCGATGCCATTAA   1153

Query   459  ATCTGAAATGAAACC   473
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Sbjct   1154  ATCTGAAATGAAACC   1168

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Query	339	TTTTG-AGGTGACAAAGTTTGCAC	TTTTGGAGACCATAAAAGAAGCAGTACCTGAAATGT	397
Sbjct	953	TTTTGTAGGTGACAAGGTTTGCAC	TTTTGGAGACCATAAAGGAAGCAGTACCAGAAATGT	1012
Query	398	GGTACCGGCTATGAAGAATGCATGGGGAGAAGCTTATGATCAGTTGGTCAATGCAATCA		457
Sbjct	1013	GGTCACCTGAGATGAAGAACGCATGGGGAGAAGCTTATGATCAGTTGGTTGCTGCTATCA		1072
Query	458	AAT-CTGAAATGAAACCTTCC	477	

Sbjct 1073 AGTTC-GAAGTGAAACCTCC 1092

>gb|AF027215.1|AF027215 Tremas orientalis hemoglobin gene, complete cds
Length=1101

Score = 158 bits (85), Expect = 4e-35
Identities = 123/141 (88%), Gaps = 3/141 (2%)
Strand=Plus/Plus

```
Query 339 TTTTG-AGGTGACAAAGTTTGCACCTTTTGGAGACCATAAAAAGAAGCAGTACCTGAAATGT 397
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct 953 TTTGTAGGTCACAAGGTTTGCACCTTTTGGAGACCATAAAGGAAGCAGTACCAGAAATGT 1012

Query 398 GGTCACCGGCTATGAAGAATGCATGGGGAGAAGCTTATGATCAGTTGGTCAATGCAATCA 457
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct 1013 GGTCACCTGAGATGAAGAACGCATGGGGAGAAGCTTATGATCAGTTGGTTGCTGCTATCA 1072

Query 458 AAT-CTGAAATGAAACCTTCC 477
          ||||| ||||| ||||| |||||
Sbjct 1073 AGTTC-GAAGTGAAACCTCC 1092
```

>emb|AJ131351.1| Tremas virgata gene encoding hemoglobin, isolate T4
Length=1104

Score = 145 bits (78), Expect = 3e-31
Identities = 120/140 (86%), Gaps = 3/140 (2%)
Strand=Plus/Plus

```
Query 340 TTTG-AGGTGACAAAGTTTGCACCTTTTGGAGACCATAAAAAGAAGCAGTACCTGAAATGTG 398
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct 957 TTTGTAGGTCACAAGGTTTGCACCTTTTGGAGACCATAAAGGAAGCGGTACCAGAAATGTG 1016

Query 399 GTCACCGGCTATGAAGAATGCATGGGGAGAAGCTTATGATCAGTTGGTCAATGCAATCAA 458
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct 1017 GTCAGCTGAGATGAAGAACGCATGGGGAGAAGCTTATGATCAGTTGGTTGCTGCTATCAA 1076

Query 459 AT-CTGAAATGAAACCTTCC 477
          ||||| ||||| ||||| |||||
Sbjct 1077 GTTC-GAAGTGAAACCTCC 1095
```

>emb|AJ131350.1| Tremas virgata gene encoding hemoglobin, isolate T2
Length=1104

Score = 145 bits (78), Expect = 3e-31
Identities = 120/140 (86%), Gaps = 3/140 (2%)
Strand=Plus/Plus

```
Query 340 TTTG-AGGTGACAAAGTTTGCACCTTTTGGAGACCATAAAAAGAAGCAGTACCTGAAATGTG 398
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct 957 TTTGTAGGTCACAAGGTTTGCACCTTTTGGAGACCATAAAGGAAGCGGTACCAGAAATGTG 1016

Query 399 GTCACCGGCTATGAAGAATGCATGGGGAGAAGCTTATGATCAGTTGGTCAATGCAATCAA 458
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct 1017 GTCAGCTGAGATGAAGAACGCATGGGGAGAAGCTTATGATCAGTTGGTTGCTGCTATCAA 1076

Query 459 AT-CTGAAATGAAACCTTCC 477
          ||||| ||||| ||||| |||||
Sbjct 1077 GTTC-GAAGTGAAACCTCC 1095
```

>emb|AJ131349.1| Tremas virgata gene encoding hemoglobin, isolate T1
Length=1103

Score = 145 bits (78), Expect = 3e-31
Identities = 120/140 (86%), Gaps = 3/140 (2%)
Strand=Plus/Plus

```
Query 340 TTTG-AGGTGACAAAGTTTGCACCTTTTGGAGACCATAAAAAGAAGCAGTACCTGAAATGTG 398
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct 956 TTTGTAGGTCACAAGGTTTGCACCTTTTGGAGACCATAAAGGAAGCGGTACCAGAAATGTG 1015

Query 399 GTCACCGGCTATGAAGAATGCATGGGGAGAAGCTTATGATCAGTTGGTCAATGCAATCAA 458
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct 1016 GTCAGCTGAGATGAAGAACGCATGGGGAGAAGCTTATGATCAGTTGGTTGCTGCTATCAA 1075

Query 459 AT-CTGAAATGAAACCTTCC 477
          ||||| ||||| ||||| |||||
Sbjct 1076 GTTC-GAAGTGAAACCTCC 1094
```